

AMENDMENTS TO THE CLAIMS:

Please replace the claims with the claims provided in the listing below wherein status, amendments, additions and cancellations are indicated.

1. (Cancelled).

2. (Currently Amended) A method to predict the topology of the spatial arrangement of an amino acid sequence comprising:

using an entropy evaluation model that takes into account the global contributions of entropy to the folding of a protein (herein referred to by the name cross linking entropy (CLE) model) combined with other thermodynamic potentials as a protein-folding model to predict said topology, A method- according to claim 1, wherein using said entropy evaluation model to predict said topology comprises the following steps:

- A. inputting an amino acid sequence of said protein,
- B. preparing information on secondary structure of said amino acid sequence
by way of at least one theoretical or experimental estimate,
- C. applying the CLE model to said amino acid sequence and secondary
structure information to evaluate the free energy of a combinatorial

number of β -strand and α -helix arrangements as rapidly as polynomial time: $c(n-1)(n+1)$ wherein c is a constant and n is the number of secondary structure elements found in the said amino acid in step A and prepared in step B,

- D. applying the CLE model in conjunction with other thermodynamic potentials that approximate hydrophobic, electrostatic and polar interactions, but not limited to these aforementioned thermodynamic potentials stated herein, in a thermodynamic calculation to account for both short and long range folding interactions and predict a minimum free energy and corresponding topology of the said amino acid sequence,
- E. applying the CLE model to predict the global folding kinetics of the said amino acid sequence, and
- F. storing the information in a data file or in other form of digital memory.

3. (Currently Amended) A method according to claim [[1 or]] 2, in which the cross linking entropy (CLE) model[[,]] is used to evaluate the entropy loss of said protein due to folding into a particular topology given a known secondary or estimated secondary structure.

4. (Previously Presented) A method according to claim 3, in which an initial theoretical estimate of the secondary structure is obtained from either a theoretical source, or an experimental source.

5. (Previously Presented) A method according to claim 4, in which said experimental source is an NMR experiment or x-ray crystallography, or both.

6. (Previously Presented) A method according to claim 5, in which the theoretical estimate is further supplemented with sequence alignment to find regions in which conserved segments remain essentially unchanged by differences in the aligned sequences.

7. (Currently Amended) A method to predict the topology of the spatial arrangement of an amino acid sequence, comprising:
using an entropy evaluation model that takes into account the global contributions of entropy to the folding of a protein (herein referred to by the name cross linking entropy (CLE) model) combined with other thermodynamic potentials as a protein-folding model to predict said topology, wherein

the cross linking entropy (CLE) model is used to evaluate the entropy loss of said protein due to folding into a particular topology given a known secondary or estimated secondary structure,

an initial theoretical estimate of the secondary structure is obtained from either a theoretical source, or an experimental source,

said experimental source is an NMR experiment or x-ray crystallography, or both, and

~~A method according to claim 5 in which~~ said amino acid sequence and secondary structure information is used to evaluate the free energy of a combinatorial number of β -strand and α -helix arrangements as rapidly as polynomial time: $c(n-1)(n+1)$, wherein c is a constant and n is the number of secondary structure elements found in the said amino acid and obtained; and further comprising storing the information in a data file or in other form of digital memory.

8. (Currently Amended) A method to predict the topology of the spatial arrangement of an amino acid sequence comprising the following steps:

- A. inputting an amino acid sequence of a protein,
- B. preparing information on secondary structure of said amino acid sequence by way of at least one theoretical or experimental estimate,

C. applying a CLE model to approximate the global folding

kinetics of the said amino acid sequence,

D. applying the CLE model to said amino acid sequence and secondary

structure information to reduce the combinatorial number of β -strand

and α -helix arrangements, and

E. applying the CLE model in conjunction with other thermodynamic

potentials that approximate hydrophobic, electrostatic and polar

interactions, but not limited to these aforementioned thermodynamic

potentials stated herein, in a thermodynamic calculation to optimize the

free energy to find the most thermodynamically favorable topology for

said amino acid sequence,

wherein the global free energy (FE) contribution from the CLE between two

distinct amino acid residues, herein labeled i and j , is calculated by

equation (1):

$$\Delta G_{ij}^{gcle} = -T\Delta S_{ij}^{gcle} = \frac{\gamma k_B T}{\xi} \left\{ \ln \left(\frac{2\gamma\xi\Delta N_{ij}}{3\lambda_{ij}^2} \right) - 1 + \frac{3\lambda_{ij}^2}{2\gamma\xi\Delta N_{ij}} \right\} \quad (1)$$

wherein, i and j represent the indices of two distinct residues in said amino acid sequence, and $j > i$, $\Delta N_{ij} = j - i + 1$ expresses the number of residues separating i and j , ΔG_{ij}^{gcle} is the difference in the free energy contribution to the global CLE from residues i and j transitioning from the denatured (random flight) state to the native state, ΔS_{ij}^{gcle} is the corresponding global entropy loss, ξ is the persistence length, γ is a dimensionless weight parameter describing the self-avoiding properties of a polymer chain, k_B is the Boltzmann constant, T is the temperature, and λ_{ij} (the bond gap) expresses the amino acid separation distance between the center of mass of residue i and the center of mass of residue j when both are treated as isolated molecules[[]], and

F. storing the information in a data file or in other form of digital memory.

9. (Currently Amended) A method to predict the topology of the spatial arrangement of an amino acid sequence comprising the following steps:

A. inputting an amino acid sequence of a protein,

B. preparing information on secondary structure of said amino acid

sequence by way of at least one theoretical or experimental estimate,

C. applying a CLE model to approximate the global folding

kinetics of the said amino acid sequence,

D. applying the CLE model to said amino acid sequence and secondary

structure information to reduce the combinatorial number of β -strand

and α -helix arrangements,

E. applying the CLE model in conjunction with other thermodynamic

potentials that approximate hydrophobic, electrostatic and polar

interactions, but not limited to these aforementioned thermodynamic

potentials stated herein, in a thermodynamic calculation to optimize the

free energy to find the most thermodynamically favorable topology for

said amino acid sequence,

wherein the global free energy (FE) contribution from the CLE between two

distinct amino acid residues, herein labeled i and j , is calculated by

equation (1):

$$\Delta G_{ij}^{gcle} = -T\Delta S_{ij}^{gcle} = \frac{\gamma k_B T}{\xi} \left\{ \ln \left(\frac{2\gamma\xi\Delta N_{ij}}{3\lambda_{ij}^2} \right) - 1 + \frac{3\lambda_{ij}^2}{2\gamma\xi\Delta N_{ij}} \right\} \quad (1)$$

wherein, i and j represent the indices of two distinct residues in said amino acid sequence, and $j > i$, $\Delta N_{ij} = j - i + 1$ expresses the number of residues separating i and j , ΔG_{ij}^{gcle} is the difference in the free energy contribution to the global CLE from residues i and j transitioning from the denatured (random flight) state to the native state, ΔS_{ij}^{gcle} is the corresponding global entropy loss, ξ is the persistence length, γ is a dimensionless weight parameter describing the self-avoiding properties of a polymer chain, k_B is the Boltzmann constant, T is the temperature, and λ_{ij} (the bond gap) expresses the amino acid separation distance between the center of mass of residue i and the center of mass of residue j when both are treated as isolated molecules, and wherein ~~A method according to claim 8, in which~~ the total CLE contribution to the free energy (ΔG_{cle}) is calculated by equation (2):

$$\Delta G_{cle} = \Delta G_{\xi}^o + \sum_{all_bonds(i,j)} \Delta G_{ij}^{gcle} + \sum_{i',j'} f_{i'j'}(\xi) \quad (2)$$

wherein, ΔG_{ij}^{gcle} is defined in equation (1), i' and j' are indices specifying two secondary structure elements (α -helices or β -strands) that are joined together by the corresponding set of bonds i and j , $f_{i'j'}(\xi)$ is a positive definite penalty function used to enforce topology constraints on the minimum allowed sequence length of a loop connecting two elements of secondary structure $i' j'$ and is a function of the persistence length ξ , and ΔG_{ξ}^o is a renormalization correction and is an integral function of ξ as shown by equation (3):

$$\Delta G_{\xi}^o = \frac{(\gamma + 1/2) N k_B T}{D \xi} \int_1^{\xi} \left(\frac{\ln(x)}{(1-x)} + 1 \right) dx \quad (3)$$

wherein, ~~ξ , γ , k_B , and T mean the same as defined in claim 8~~, N indicates the number of amino acids in the said sequence, D is the dimensionality of the system, the limits in the integral ($1 \rightarrow \xi$) indicate the change in the number of degrees of freedom from an individual amino acid residue to a cluster of ξ amino acids treated as a group (where $\xi > 1$ amino acid and ξ need not be an integer) and x is a dummy variable in the integral substituting for $\xi[[.]]$, and

F. storing the information in a data file or in other form of digital memory.

10. (Previously Presented) A method according to claim 9, in which optimal β -sheet alignments are obtained by using thermodynamics.

11. (Previously Presented) A method according to any one of claims 8 to 10, in which the CLE model is applied in conjunction with other derived or constructed thermodynamic potentials that approximate hydrophobic, electrostatic and polar interactions, in a thermodynamic calculation to account for both short and long range folding interactions and predict a minimum free energy and corresponding topology of said amino acid sequence.

12. - 13. (Cancelled).